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2: /cgn2_6/ptodata/1/paa/US06_NEW_COMB.pep:*

3: /cgn2_6/ptodata/1/paa/US07_NEW_COMB.pep:*

4: /cgn2_6/ptodata/1/paa/US08_NEW_COMB.pep:*

5: /cgn2_6/ptodata/1/paa/US09_NEW_COMB.pep:*

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## APPLICANT: Fling, Steven P. APPLICANT: Xu, Jiangchun TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THE TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER FILE REFERENCE: 210121.48406 CURRENT APPLICATION UMBER: US/09/970,966 CURRENT FILING DATE: 2001-10-02 NUMBER OF SEQ ID NOS: 215 SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 209 LENGTH: 453 QY ρy В Qy DЬ QY Вþ QY 밁 밁 QΥ ; ORGANISM: Homo sapiens US-09-970-966-209 Query Match Best Local : Matches 453; TYPE: PRT 301 181 241 241 181 121 121 61 61 KGYLQKEVTDHMVSLACSDILVFLIGMPMEFYSIIWNPLTTSSYTLSCKLHTFLFEACSY 120 Local Similarity VNVPSHRGLTCNRSSTRHHEQPETSNMSICTNLSSRWTVFQSSIFGAFVVYLVVLLSVAF MCWNMMQVLMKSQKGSLAGGTRPPQLRKSESEESRTARRQTIIFLRLIVVTLAVCWMPNQ ATLLHYLTLSEBRYIAICHPFRYKAVSGPCQVKLLIGFVWVTSALVALPLLFAMGTEYPL IRRIMAAAKPK#DWTRSYFRAYMILLPFSETFFYLSSVINPLLYTVSSQQFRRVFVQVLC IRRIMAAAKPKHDWTRSYFRAYMILLPFSETFFYLSSVINPLLYTVSSQQFRRVFVQVLC ${\tt MCWNMMQVLMKSQKGSLAGGTRPPQLRKSESEESRTARRQTIFLRLIVVTLAVCWMPNQ}$ VNVPSHRGLTCNRSSTRHHEQPETSNMSICTNLSSRWTVFQSSIFGAFVVYLVVLLSVAF ATLLHVLTLSFERYIAICHPFRYKAVSGPCQVKLLIGFVWVTSALVALPLLFAMGTEYPL KGYLQKEVTDHMVSLACSDILVFLIGMPMEFYSIIWNPLTTSSYTLSCKLHTFLFEACSY 120 100.0%; ilarity 100.0%; Conservative 0 0; Score 2334; DB 5; Pred. No. 2.4e-197; Mismatches Length 453; Indels THERAPY 0;

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Matches 107; Conserv
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LENGTH: 410
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APPLICANT: Erding I
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CURRENT APPLICATION NUMBER: US/09/988,922
CURRENT FILING DATE: 2001-11-19
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SOFTWARE: FastSEQ for Win
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Yuan Zhu
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Stephane Clement Krief
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Erin M. Toland
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Joyce Yue Mao
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Han Ngoc Trinh
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Randall Forrest Smith
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Melanie Robbins
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                                                                                            Conservative
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PRIOR FILING DATE: 1999-02-26
PRIOR APPLICATION NUMBER: 60/109,213
PRIOR FILING DATE: 1998-11-20
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PRIOR FILING DATE: 1998-10-13
PRIOR APPLICATION NUMBER: 60/110,060
PRIOR FILING DATE: 1998-11-27
PRIOR APPLICATION NUMBER: 60/120,416
PRIOR FILING DATE: 1999-02-16
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                                                                  PRIOR APPLICATION NUMBER: 60/108,029
PRIOR FILING DATE: 1998-11-12
PRIOR APPLICATION NUMBER: 60/136,436
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CURRENT FILING DATE: 2001-06-07
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R APPLICATION NUMBER: 60/151,114
R FILING DATE: 1999-08-27
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Liaw, Chen W.
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NUMBER: 60/136,439
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APPLICATION NUMBER: 60/136,567 FILING DATE: 1999-05-28 APPLICATION NUMBER: 60/137,127 FILING DATE: 1999-05-28

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               APPLICANT: Chen, Ruoping APPLICANT: Dang, Huong applicant: Liaw, Chen W
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                                                                                                                                                                                                                                                                                                                                               269 SESEESRTARRQTIIFLRLIVVTLAVCWMPNQIRRIMAAAKPKHDWTRSYFRAYMILLPF 328
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APPLICATION NUMBER: 60/157,280
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Lin, I-Lin
                    Dang, Huong T
Liaw, Chen W.
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Best Local
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PRIOR FILING DATE: 1999-05-28
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PRIOR FILING DATE: 1999-10-01
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TYPE: PRT
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Local Similarity 28.0%;
es 97; Conservativo
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NLSSRWT----VFQSSIFGAFVVYLVVLLSVAFMCWNMMQVLMKSQKGSLAGGTRPPQLRK 268
                                                                 ILGIVWGFSVLFSLP-----
                                                                                                   LIGFVWVTSALVALPLLFAMGTEYPLVNVPSHRGLTCNRSSTRHHEQPETS---NMSICT 211
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                                                                 -NTSIH-----GIKFHYFPNGSLVPGSATCT 205
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US-09-876-252-130
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PRIOR FILING DATE: 1999-03-12
(OR APPLICATION NUMBER: 60/123,946
(OR FILING DATE: 1999-03-12
PRIOR FILING DATE: 1999-03-12
PRIOR FILING DATE: 1999-03-12
PRIOR APPLICATION NUMBER: 60/152,524
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CURRENT APPLICATION NUMBER: US/09/876,252
CURRENT FILING DATE: 2001-06-07
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                                                                                                                                      APPLICATION NUMBER: FILING DATE: 1999-05
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APPLICATION NUMBER: 60/:
FILING DATE: 1999-05-28
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APPLICATION NUMBER: 60/151,114
FILING DATE: 1999-08-27
                                                                FILING DATE: 1999-06-29
APPLICATION NUMBER: 60/136,437
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FILING DATE:
                       APPLICATION NUMBER: 60/156,555
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APPLICATION NUMBER: 60/123,945
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Liaw, Chen W.
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Chalmers, Derek T.
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Best Local Similarity 28.5%;
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                                               SEQ ID NO 114
                                                                                                                                                                                                                                                                                                                              Sequence 114, Application US/09170496D
                                                                CURRENT APPLICATION NUMBER: US/09/170,496D
CURRENT FILING DATE: 1998-10-13
NUMBER OF SEQ ID NOS: 294
SOFTWARE: Patentin version 3.1
                                                                                                                                                              APPLICANT: Behan, Dominic P.
APPLICANT: Chalmers, Derek T.
APPLICANT: Liaw, Chen W.
TITLE OF INVENTION: Non-Endogenous, Constitutively Activated
TITLE OF INVENTION: Receptors
FILE REFERENCE: AREN-0040
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PRIOR FILING DATE: 1999-09-29
PRIOR APPLICATION NUMBER: 60/156,653
PRIOR FILING DATE: 1999-09-29
PRIOR APPLICATION NUMBER: 60/157,280
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    180 LVN-VPSHRGLTCNRSSTRHHEQ------PETSNMSICTNLSSRWTVFQSS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 KGYLQKEVTDHMVSLACSDILVFLIGMPMEFYSIIWNPLTTSSYTLSCKLHTFLFEACSY 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20 PALPPCDERRCS-----PFPLGALVPVT--AVCLCLFVVGVSGNVVTV---MLIGR 65
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APPLICATION NUMBER: 60/157,294
FILING DATE: 1999-10-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: 60/157,282
FILING DATE: 1999-10-01
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US-09-170-496D-224
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/09/170,496D
RRENT FILING DATE: 1998-10-13
MBER OF SEQ ID NOS: 294
SOFTWARE: PatentIn version 3.1
SEQ ID NO 224
SEQ ID NO 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 224, Application US/09170496D GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: Non-Endogenous, Constitutively Activated Human G Protein-Coupled TITLE OF INVENTION: Receptors FILE REFERENCE: AREN-0040
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Behan, Dominic P. APPLICANT: Chalmers, Derek T. APPLICANT: Liaw, Chen W.
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TYPE: PRT
ORGANISM: Homo sapiens
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150 VTRAHVRRVLGAVWGLAMLCSLPNTSLHGIRQ--LHVPC-RG------
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                                                                                                                                                          91 LPLELYE-MWHNYPFLLGVGGCYFRTLLFEMVCLASVLNVTALSVERYVAVVHPLQARSM 149
                                                                                                                                                                                                                                                                                                                         34 TELFMPICATYLLIFVVGAVGNGLTCLV--ILRHKA-MRTPTNYYLFSLAVSDLLVLLVG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
nes 104; Conserv
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                                                                                                                                                                                                                                       MPMEEYSIIWNPLTTSSYTLSCKLHTELEEACSYATLLHVLTLSFERYIAICHPFRYKAV 146
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; SEQ ID NO 26
; LENGTH: 419
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
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; Sequence 26, Application US/09804551B
; GENERAL INFORMATION:
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Best Local Similarity
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340 TCINPLLYNIMSHKFREAFKAVLFGKKVSKGSLNSRNNIESRRLRRALTNSSQTQRF 396
                                             337 SVINPLLYTVSSQQFRRVFVQVL----CCRLSLQHANH--EKRLRVHAHSTTDSARF 387
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                                                                                                                                                                                                                                                                                                                                       204 TSNMSICTNLSSRWTVFQSSIFGAFV----VYLVVLLSVAFMCWNMMQV-----LMKSQK 254
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                                                                                                                                        285 LRLIVVTLAVCWMPNQIRRIMAAAKP------KHDWTRSYFRAYMILLPFSETFFYLS 336
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     29 IKITLILVYLIIFVMGLLGNSATIRVTQVLQKKGYLQKEVTDHMVSLACSDILVFLIGMP 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QE-VSYIWSKYPYVFGEYI--CIGRGLLAETSANATVLTITAFTVERYIAICHPFLGQAM 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEFYSIIWN--PLTTSSYTLSCKLHTFLFEACSYATLLHVLTLSFERYIAICHPFRYKAV 146
                                                                                             LVAVVVCFFLCWAPFHAQRLIAIYAPARGAKLRDQHEF-----VYTVMTYVSGVLYYLS 339
                                                                                                                                                                                          LKSVPSDTILYRYGGSGTAMSFNGGGSGAGTAGLMGGSGAQLSSVRGRLNHYGTRRVLRM 285
                                                                                                                                                                                                                                          ----GTRPPQLRKSESEESRTARRQTIIF 284
                                                                                                                                                                                                                                                                                       -----FQLSTFIFFLAPMSIILVLYLLIGVHLYRSTLVEGPASVARRQQ 225
                                                                                                                                                                                                                                                                                                                                                                                       SKLSRAIRIIVLVWIMAIVTAIPQAAQFGIEH-----YSGVEQCGIVRVIVKHS---- 181
                                                                                                                                                                                                                                                                                                                                                                                                                                  SGPCQVKLLIGFVWVTSALVALPLLFAMGTEYPLVNVPSHRGL-TCN--RSSTRHHEQPE 203
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16;

RESULT 9 US-09-170-496D-88

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ORGANISM: Homo sapiens US-09-170-496D-88
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                                                                                  ; ORGANISM: Homo sapiens US-09-170-496D-210
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 88, Application US/09170496D GENERAL INFORMATION:
                                                                                                                    NUMBER OF SEQ ID NOS: 294
SOFTWARE: PatentIn version 3.1
SEQ ID NO 210
LENGTH: 366
TYPE: PRT
                                                                                                                                                                                                                                                                                    Sequence 210, Application US/09170496D GENERAL INFORMATION:
APPLICANT: Behan, Dominic P.
APPLICANT: Chalmers, Derek T.
APPLICANT: Liaw, Chen W.
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Best Local Similarity
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                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/09/170,496D CURRENT FILING DATE: 1998-10-13
                                                                                                                                                                                                                                                      TITLE OF INVENTION: Non-Endogenous, Constitutively Activated Human G Protein-Coupled TITLE OF INVENTION: Receptors
                                                                                                                                                                                                                                      FILE REFERENCE: AREN-0040
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nes 93; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WVTSALVALPLLFAMGTEYPLVNVPSHRGLTCNRSSTRHHEQPETSNMSICTNLSSR--- 216
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Conservative
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                 12.6%; score 293; DB 5; 27.8%; Pred. No. 2.9e-18;
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   59;
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Pred. No. 8.7e-19;
0; Mismatches 118
   Mismatches
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; TYPE: PRT
; ORGANISM: HOMO
US-09-611-526-3507
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US-09-611-526-3507
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CURRENT ELLING DATE: 2000-07-07
PRIOR APPLICATION NUMBER: JP 1999-194486
PRIOR FILING DATE: 1999-07-08
PRIOR APPLICATION NUMBER: JP 2000-118774
PRIOR APPLICATION NUMBER: JP 2000-118774
PRIOR FILING DATE: 2000-01-11
PRIOR APPLICATION NUMBER: JP 2000-183765
PRIOR FILING DATE: 2000-05-02
NUMBER OF SEQ ID NOS: 4484
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                                                                                                                                                                                                                                     SOFTWARE: PatentIn Ver. SEQ ID NO 3507 LENGTH: 380
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APPLICANT:
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GGDFDNYYGADNOSECEYTDWKSSGALIPAIYMLVFLLGTTGNGLVL--WTVFRSSREKR
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SUGIYAMA, TOMOYASU
NAGAI, KEIICHI
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OTSUKI, TETSUJI
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KAWAI, YURI
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HAYASHI, KOJI
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                                                                            11.8%; Score 276.5; DB 5; 24.9%; Pred. No. 8.6e-17; tive 61; Mismatches 154;
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APPLICANT: Behan, Dominic P.
APPLICANT: Chalmers, Derek T.
APPLICANT: Liaw, Chen W.
APPLICANT: Liaw,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQ ID NOS: 294
SOFTWARE: PatentIn version 3.1
SEQ ID NO 62
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              66 KEVTDHMVSLACSDILVFLIGMPMEFYSIIWNPLTTSSY-----TLSCKLHTFLFEACSY 120
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                                                                                                                                                                                                                   LAVCWMPNQIRRIMAAAKPKHDWTRSYFRAYMILLPFSETFFYLSSVINPLLYTVSSQQF 351
RQACTSMLCC 326
                                                                      RRVFVQVLCC 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ch 11.7%; Score 272.5; DB 5; Cl Similarity 24.6%; Pred. No. 1.9e-16; 91; Conservative 62; Mismatches 154;
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; TYPE: PRT; ORGANISM: Homo sapiens US-09-170-496D-198
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US-09-170-496D-198
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SOFTWARE: PatentIn version 3.1
SEQ ID NO 198
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TITLE OF INVENTION: A NOVEL HUMAN G-PROTEIN COUPLED RECEPTOR, HGPRBMY18, TITLE OF INVENTION: EXPRESSED HIGHLY IN PITUITARY GLAND AND COLON CARCII TITLE OF INVENTION: CELLS FILE REFERENCE: D0048up CURRENT APPLICATION NUMBER: US/09/992,331 CURRENT FILING DATE: 2001-11-14 PRIOR APPLICATION NUMBER: 60/308,540 PRIOR APPLICATION NUMBER: 60/261,782 PRIOR APPLICATION NUMBER: 60/261,782
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILE REFERENCE: AREN-0040 CURRENT APPLICATION NUMBER: US/09/170,496D
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                                                                                                                                                                                                                                                                                                                             APPLICANT: FEDER, JOHN N. APPLICANT: MINTIER, GABE
                                                                                                                                                                                                                                                                        APPLICANT: RAMANATHAN, CHANDRA S. APPLICANT: HAWKEN, DONALD R.
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25.1%; Pred. No. 1.9e-16;
tive 60; Mismatches 154
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PRIOR FILING DATE: 2001-01-16

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PRIOR APPLICATION NUMBER: 60/248,483

PRIOR FILING DATE: 2000-11-14

NUMBER OF SEQ ID NOS: 45

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 19

LENGTH: 444

TYPE: PRT

ORGANISM: Homo sapiens
US-09-992-331-19
CURRENT APPLICATION NUMBER: US/09/595,549
CURRENT FILING DATE: 2000-06-16
PRIOR APPLICATION NUMBER: US/926812
PRIOR FILING DATE: 1998-12-17
PRIOR APPLICATION NUMBER: 60/069,725
PRIOR FILING DATE: 1997-12-17
NUMBER OF SEQ ID NOS: 16
SEQ ID NO 6
SEQ ID NO 6
LENGTH: 346
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Best Local Similarity
Watches 99; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 6, Application US/09595549
GENERAL INFORMATION:
APPLICANT: Howard, Andrew D.
APPLICANT: Cascieri, Margaret A.
                                                                                                                                                                                                                       APPLICANT: Tan, Carina
APPLICANT: Van der Ploeg, Leonardus H. T.
APPLICANT: Lynch, Kevin R.
TITLE OF INVENTION: GALANIN RECEPTOR GALR3 AND
TITLE OF INVENTION: ENCODING SAME
FILE REFERENCE: 20148PCA
                                                                                                                                                                                                                                                                                                                                       APPLICANT:
APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                301 KTARMLMYVLLVFAICYLPISILNVLKRVFGMFAHTEDRETVYAWF-----TFSHWLV 353
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           203 -----KTTLFTVC---DERWGGEIYPKMYHICFF--LVTYMAPLCLMVLAYLQI 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    154 YAICHPLMFKSTAKRARNSIVI -- IWIVSCIIMIPQAIVMECSTVFPGLAN------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              135 IAICHPFRYKAVSGPCQVKLLIGFVWVTSALVALPLLFAM--GTEYP-LVNVPSHRGLTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                76 ACSDILVFLIGMPMEFYSIIWNPLTTSSYTLS-CKLHTFLFEACSYATLLHVLTLSFERY 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               46 EYLHPKEYE---WV---LIAGYIIVFVVALIGN---VLVCVAVWKNHHMRTYTNYFIVNL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16 DHSHVPEFEVATWIKITLILVYLIIFVMGLLGNSATIRVTQVLQKKGYLQKEVTDHMVSL 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -----C------WNMMQVLMKSQKGSLAGGTRPPQLRKS----ESEESRTARR 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NRSSTRHHEQPETSNMSICTNLSSRW-----TVFQSSIFGAFVVYL--VVLLSVAFM-- 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SLADVLVTITCLPA---TLVVDITETWFFGQSLCKVIPYLQTVSVSVSVLTLSCIALDRW 153
                                                                                                                                                                                                                                                                                                                                                                                   Smith, Roy G
                                                                                                                                                                                                                                                                                                                                                            Sullivan, Kathleen A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11.3%; Score 263.5; DB 5; Length 444; 21.2%; Pred. No. 1.4e-15; rative 99; Mismatches 154; Indels 115;
                                                                                                                                                                                                                                                                   NUCLEOTIDES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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Best Local :
324 SPHGDAKEKNRIDTPPSTN 342
                                           367 --HANHEKRLRVHAHSTTD 383
                                                                                                                                       316 RSYFRAYMILLPFSETFF-----YLSSVINPLLYTVSSQQFRRVFVQVLCCRLSLQ 366
                                                                                                                                                                                                                                  256 SLAGGTRPPQLRKSESEESRTARRQTIIFLRLIVVTLAVCWMPNQIRRIMAAAKPKHDWT 315
                                                                                                                                                                                                                                                                                     179 ---DSNQTFCWEHWPNQLHKKAYVVCTFVFG----YLLPLLLICFCYAKVLNHLHKKLKN 231
                                                                                                                                                                                                                                                                                                                                                                               140 RRSSSLRVSRNALLGVGFIWALSIAMASPVAY----YQRL---FHR------
                                                                                                                                                                                          232 -----MSKKSEASKKKTA--QTVL---VVVVVFGISWLPHHV-----IHLWA 268
                                                                                                                                                                                                                                                                                                                              201 QPETSNMSIC-----TNLSSRWTVFQSSIFGAFVVYLVVLLSVAFMCWNMMQVLMKSQKG 255
                                                                                                                                                                                                                                                                                                                                                                                                                                  141 FRYKAVSGPCQVKLLIGFVWVTSALVALPLLFAMGTEYPLVNVPSHRGLTCNRSSTRHHE 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  82 AYLLECIP--FQATVYALPTWVLGAFICKFIHYFFTVSMLVSIFTLAAMSVDRYVAIVHS 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             81 LVFLIGMPMEFYSIIWNPLTTSSYTLSCKLHTFLFEACSYATLLHVLTLSFERYIAICHP 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                24 PLFGIGVENFITLV-VFGLIFAMGVLGNSLVITVL-ARSKPGKPRSTTNLFILNLSIADL 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21 PEFEVATWIKITLILVYLIIFVMGLLGNSATIRVTQVLQKKGYLQKEVTDHMVSLACSDI 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local
                                                                                         E--FGAFP-LTPAS--FFFRITAHCLAYSNSSVNPIIYAFLSENFRKAYKQVFKCRVCNE 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    94;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            h 11.1%; Score 258; DB 5; Length 346; Similarity 24.8%; Pred. No. 3.2e-15; 94; Conservative 68; Mismatches 141; Indels 76;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                    178
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23;

Search completed: January 8, 2002, 23:09:49 Job time: 384 sec

